

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/531164  
Source: PC  
Date Processed by STIC: 5-3-05

# ***ENTERED***



PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/531,164

DATE: 05/03/2005  
TIME: 11:39:36

Input Set : D:\819\_seq\_listing.txt  
Output Set: N:\CRF4\05032005\J531164.raw

6 <110> APPLICANT: Tang, Y. Tom  
7 Wang, Jian-Rui  
8 Wang, Zhiwei  
9 Zhou, Ping  
10 Zhang, Jie  
11 Ghosh, Malabika  
12 Ren, Feiyan  
13 Asundi, Vinod  
14 Zhao, Qing A.  
15 Xue, Aidong J.  
16 Chen, Rui-hong  
17 Wehrman, Tom  
18 Ma, Yunging  
19 Wang, Dunrui  
20 Weng, Gezhi  
23 <120> TITLE OF INVENTION: Novel Nucleic Acids and  
24 Polypeptides  
28 <130> FILE REFERENCE: 819CIP/PCT  
C--> 30 <140> CURRENT APPLICATION NUMBER: US/10/531,164  
C--> 31 <141> CURRENT FILING DATE: 2005-04-12  
33 <150> PRIOR APPLICATION NUMBER: 60/416,186  
34 <151> PRIOR FILING DATE: 2002-10-02  
36 <150> PRIOR APPLICATION NUMBER: PCT/US00/35017  
37 <151> PRIOR FILING DATE: 2000-12-22  
39 <150> PRIOR APPLICATION NUMBER: PCT/US01/02623  
40 <151> PRIOR FILING DATE: 2001-01-25  
42 <150> PRIOR APPLICATION NUMBER: PCT/US01/03800  
43 <151> PRIOR FILING DATE: 2001-02-05  
45 <150> PRIOR APPLICATION NUMBER: PCT/US01/04927  
46 <151> PRIOR FILING DATE: 2001-02-26  
48 <150> PRIOR APPLICATION NUMBER: PCT/US01/04941  
49 <151> PRIOR FILING DATE: 2001-03-05  
51 <150> PRIOR APPLICATION NUMBER: PCT/US01/08631  
52 <151> PRIOR FILING DATE: 2001-03-30  
54 <150> PRIOR APPLICATION NUMBER: PCT/US01/08656  
55 <151> PRIOR FILING DATE: 2001-04-18  
57 <150> PRIOR APPLICATION NUMBER: 10/084,643  
58 <151> PRIOR FILING DATE: 2002-02-26  
62 <160> NUMBER OF SEQ ID NOS: 2564  
64 <170> SOFTWARE: pt\_FL\_genes Version 6.0  
70 <210> SEQ ID NO: 1  
71 <211> LENGTH: 1239  
72 <212> TYPE: DNA

(pg. 6-7)

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73 <213> ORGANISM: Homo sapiens
75 <220> FEATURE:
76 <221> NAME/KEY: CDS
77 <222> LOCATION: (58)..(579)
79 <400> SEQUENCE: 1
80 cggcacgagc gactccccgc accactcagg gtcctgtgga cagctcacct agcggca      57
81 atg gct gca ggc tcc cgg acg tcc ctg ctc ctg gct ttt gcc ctg ctc      105
82 Met Ala Ala Gly Ser Arg Thr Ser Leu Leu Ala Phe Ala Leu Leu
83   1           5           10           15
85 tgc ctg ccc tgg ctt caa gag gct ggt gcc gtc caa acc gtt ccc tta      153
86 Cys Leu Pro Trp Leu Gln Glu Ala Gly Ala Val Gln Thr Val Pro Leu
87           20           25           30
89 tcc agg ctt ttt aaa gag gct atg ctc caa gcc cat cgc gca cac cag      201
90 Ser Arg Leu Phe Lys Glu Ala Met Leu Gln Ala His Arg Ala His Gln
91           35           40           45
93 ctg gcc att gac acc tac cag gag ttt ata agc tct tgg gga atg ggt      249
94 Leu Ala Ile Asp Thr Tyr Gln Glu Phe Ile Ser Ser Trp Gly Met Gly
95           50           55           60
97 gcg ggt cag ggg tgg caa gaa ggg gtg act ttc ccc cac tgg gga agt      297
98 Ala Gly Gln Gly Trp Gln Glu Gly Val Thr Phe Pro His Trp Gly Ser
99           65           70           75           80
101 aat ggg agg aga cta agg agc tca ggg ttg ttt tct gaa gcg aaa atg      345
102 Asn Gly Arg Arg Leu Arg Ser Ser Gly Leu Phe Ser Glu Ala Lys Met
103           85           90           95
105 cag gca gat gag cat agg ctg agc cag gtt ccc aga aga gta aca gtg      393
106 Gln Ala Asp Glu His Arg Leu Ser Gln Val Pro Arg Arg Val Thr Val
107           100          105          110
109 gga gct ggt ctc cag cat aga aag cag tgg tcc ttc ttg gtg ggg ggt      441
110 Gly Ala Gly Leu Gln His Arg Lys Gln Trp Ser Phe Leu Val Gly Gly
111           115          120          125
113 cct tcc cct agg aag aag cct ata tca caa agg aac aga agt att cat      489
114 Pro Ser Pro Arg Lys Lys Pro Ile Ser Gln Arg Asn Arg Ser Ile His
115           130          135          140
117 tcc tgc atg act ccc aga cct cct tct gct tct cag act cta ttc cga      537
118 Ser Cys Met Thr Pro Arg Pro Pro Ser Ala Ser Gln Thr Leu Phe Arg
119           145          150          155          160
121 cat cct cca aca tgg agg aaa cgc agc aga aat cca act tag agtgct      586
122 His Pro Pro Thr Trp Arg Lys Arg Ser Arg Asn Pro Thr
123           165          170
125 ccacatctcc ctgctgctca tcgagtcgcg gctggagccc gtgcgggtcc tcaggagtac      646
127 cttcaccaaac aacctggtgt atgacacctc ggacagcgat gactatcacc tcctaaagga      706
129 cctagaggaa ggcattcaaa tgctgatggg ggtgaggggtg gcaccagggg tccccaatcc      766
131 tggaagccca ctggcttcga gggctggggg agagaaacac tgctgccctc ttttcagcag      826
133 tcaggcgctg acccaagaga actcacctta ttcttcattt cccctcgtga atcctccagg      886
135 cctttctcta caccctgaag gggaaggagg aaaatggata aatgagagag ggaggggaaca      946
137 gtgccaagc gcttggtctc tccttctctt gcttcacttt gcagaggctg gaagacggca      1006
139 gccacctgac tgggcagacc ctcaagcaga cctacagcaa gtttgacaca aactcgcaca      1066
141 accatgacgc actgctcaag aactacgggc tgctccactg cttcaggaag gacatggaca      1126
143 aggtcgagac attcctgcgc atggtgcagt gccgctctgt ggagggcagc tgtggcttct      1186

```

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```

145 aggggccccgc gtggcatcct gtgacccccccc cccagccccccc ccctcgccct gca 1239
150 <210> SEQ ID NO: 2
151 <211> LENGTH: 1015
152 <212> TYPE: DNA
153 <213> ORGANISM: Homo sapiens
155 <220> FEATURE:
156 <221> NAME/KEY: CDS
157 <222> LOCATION: (58)..(828)
159 <400> SEQUENCE: 2
160 cggcagcagc gactccccgc accactcagg gtccctgtgga cagctcacct agcggca 57
161 atg gct gca ggc tcc cgg acg tcc ctg ctc ctg gct ttt gcc ctg ctc 105
162 Met Ala Ala Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Ala Leu Leu
163 1 5 10 15
165 tgc ctg ccc tgg ctt caa gag gct ggt gcc gtc caa acc gtt ccc tta 153
166 Cys Leu Pro Trp Leu Gln Glu Ala Gly Ala Val Gln Thr Val Pro Leu
167 20 25 30
169 tcc agg ctt ttt aaa gag gct atg ctc caa gcc cat cgc gca cac cag 201
170 Ser Arg Leu Phe Lys Glu Ala Met Leu Gln Ala His Arg Ala His Gln
171 35 40 45
173 ctg gcc att gac acc tac cag gag ttt gaa gaa gcc tat atc aca aag 249
174 Leu Ala Ile Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Thr Lys
175 50 55 60
177 gaa cag aag tat tca ttc ctg cat gac tcc cag acc tcc ttc tgc ttc 297
178 Glu Gln Lys Tyr Ser Phe Leu His Asp Ser Gln Thr Ser Phe Cys Phe
179 65 70 75 80
181 tca gac tct att ccg aca tcc tcc aac atg gag gaa acg cag cag aaa 345
182 Ser Asp Ser Ile Pro Thr Ser Ser Asn Met Glu Glu Thr Gln Gln Lys
183 85 90 95
185 tcc aac tta gag ctg ctc cac atc tcc ctg ctg ctc atc gag tcg cgg 393
186 Ser Asn Leu Glu Leu Leu His Ile Ser Leu Leu Leu Ile Glu Ser Arg
187 100 105 110
189 ctg gag ccc gtg cgg ttc ctc agg agt acc ttc acc aac aac ctg gtg 441
190 Leu Glu Pro Val Arg Phe Leu Arg Ser Thr Phe Thr Asn Asn Leu Val
191 115 120 125
193 tat gac acc tcg gac agc gat gac tat cac ctc cta aag gac cta gag 489
194 Tyr Asp Thr Ser Asp Ser Asp Asp Tyr His Leu Leu Lys Asp Leu Glu
195 130 135 140
197 gaa ggc atc caa atg ctg atg ggg gtg agg gtg gca cca ggg gtc ccc 537
198 Glu Gly Ile Gln Met Leu Met Gly Val Arg Val Ala Pro Gly Val Pro
199 145 150 155 160
201 aat cct gga agc cca ctg gct tcg agg gct ggg gga gag aaa cac tgc 585
202 Asn Pro Gly Ser Pro Leu Ala Ser Arg Ala Gly Gly Glu Lys His Cys
203 165 170 175
205 tgc cct ctt ttc agc agt cag gcg ctg acc caa gag aac tca cct tat 633
206 Cys Pro Leu Phe Ser Ser Gln Ala Leu Thr Gln Glu Asn Ser Pro Tyr
207 180 185 190
209 tct tca ttt ccc ctc gtg aat cct cca ggc ctt tct cta cac cct gaa 681
210 Ser Ser Phe Pro Leu Val Asn Pro Pro Gly Leu Ser Leu His Pro Glu
211 195 200 205

```

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```

213 ggg gaa gga gga aaa tgg ata aat gag aga ggg agg gaa cag tgc cca      729
214 Gly Glu Gly Gly Lys Trp Ile Asn Glu Arg Gly Arg Glu Gln Cys Pro
215      210      215      220
217 agc gct tgg tct ctc ctt ctc ttg ctt cac ttt gca gag gct gga aga      777
218 Ser Ala Trp Ser Leu Leu Leu Leu Leu His Phe Ala Glu Ala Gly Arg
219 225      230      235      240
221 cgg cag cca cct gac tgg gca gac cct caa gca gac cta cag caa gtt      825
222 Arg Gln Pro Pro Asp Trp Ala Asp Pro Gln Ala Asp Leu Gln Gln Val
223      245      250      255
225 tga caca aactcgaca accatgacgc actgctcaag aactacgggc tgctccactg      882
229 cttcaggaag gacatggaca aggtcgagac attcctgcgc atggtgcagt gccgctctgt      942
231 ggagggcagc tgtggttct aggggcccgc gtggcatcct gtgaccccc ccagcccc      1002
233 ccctcgccct gca      1015
238 <210> SEQ ID NO: 3
239 <211> LENGTH: 997
240 <212> TYPE: DNA
241 <213> ORGANISM: Homo sapiens
243 <220> FEATURE:
244 <221> NAME/KEY: CDS
245 <222> LOCATION: (64)..(120)
247 <400> SEQUENCE: 3
248 gagcatccca aggcccgact ccccgaccca ctcagggtcc tgtggacagc tcacctagcg      60
250 gca atg gct gca gga aga agc cta tat cac aaa gga aca gaa gta ttc      108
251 Met Ala Ala Gly Arg Ser Leu Tyr His Lys Gly Thr Glu Val Phe
252      1      5      10      15
254 att cct gca tga ctc ccagacctcc ttctgcttct cagactctat tccgacatcc      163
255 Ile Pro Ala
258 tccaacatgg aggaaacgca gcagaaatcc aacttagagc tgctccacat ctccctgctg      223
260 ctcacatgag cgcggctgga gcccgtgcgg ttcctcagga gtaccttcac caacaacctg      283
262 gtgtatgaca cctcggacag cgatgactat cacctcctaa aggacctaga ggaaggcatc      343
264 caaatgctga tggggaggct ggaagacggc agccacctga ctgggcagac cctcaagcag      403
266 acctacagca agtttgacac aaactcgcac aaccatgacg cactgctcaa gaactacggg      463
268 ctgctccact gcttcaggaa ggacatggac aaggtcgaga cattcctgcg catggtgcag      523
270 tgccgctctg tggagggcag ctgtggcttc taggggcccg cgtggcatcc tgtgacctct      583
272 cccagtgccc tcttccttgg gccctgaagg tgccattccc aggggcccac acaaaaggcct      643
274 ggtccttaat taacacttta acggttgga tgggccagaa aaaagagaca gaacaacaa      703
276 cgaacaacac accatttgtg gcccggcacc gacgcccaca ggaacaagcg ttgcaagaac      763
278 ccaccgcgat ggagtggacg cgcggagccg ccacagtgtg gtgaacggca gcaagggtg      823
280 ccaaaaggag gtgacccagg aggacaccgc ggcaggacac aaggggtggg ataccagca      883
282 ctataaaaaa gccgcggggg acacacgaca gctgtgtaga acaccccagc agagcgtgcc      943
284 cggaggccaa gaggacataa tcacaggagg ccacagcgac ggcgataaa tacg      997
289 <210> SEQ ID NO: 4
290 <211> LENGTH: 987
291 <212> TYPE: DNA
292 <213> ORGANISM: Homo sapiens
294 <220> FEATURE:
295 <221> NAME/KEY: CDS
296 <222> LOCATION: (1)..(771)
298 <400> SEQUENCE: 4

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299	atg gct cca ggc tcc cgg acg tcc ctg ctc ctg gct ttt gcc ctg ctc	48
300	Met Ala Pro Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Ala Leu Leu	
301	1 5 10 15	
303	tgc ctg ccc tgg ctt caa gag gct ggt gcc gtc caa acc gtt ccg tta	96
304	Cys Leu Pro Trp Leu Gln Glu Ala Gly Ala Val Gln Thr Val Pro Leu	
305	20 25 30	
307	tcc agg ctt ttt gac cac gct atg ctc caa gcc cat cgc gcg cac cag	144
308	Ser Arg Leu Phe Asp His Ala Met Leu Gln Ala His Arg Ala His Gln	
309	35 40 45	
311	ctg gcc att gac acc tac cag gag ttt gaa gaa acc tat atc cca aag	192
312	Leu Ala Ile Asp Thr Tyr Gln Glu Phe Glu Glu Thr Tyr Ile Pro Lys	
313	50 55 60	
315	gac cag aag tat tca ttc ctg cat gac tcc cag acc tcc ttc tgc ttc	240
316	Asp Gln Lys Tyr Ser Phe Leu His Asp Ser Gln Thr Ser Phe Cys Phe	
317	65 70 75 80	
319	tca gac tct att ccg aca ccc tcc aac atg gag gaa acg caa cag aaa	288
320	Ser Asp Ser Ile Pro Thr Pro Ser Asn Met Glu Glu Thr Gln Gln Lys	
321	85 90 95	
323	tcc aat cta gag ctg ctc cgc atc tcc ctg ctg ctc atc gag tcg tgg	336
324	Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Glu Ser Trp	
325	100 105 110	
327	ctg gag ccc gtg cgg ttc ctc agg agt atg ttc gcc aac aac ctg gtg	384
328	Leu Glu Pro Val Arg Phe Leu Arg Ser Met Phe Ala Asn Asn Leu Val	
329	115 120 125	
331	tat gac acc tcg gac agc gat gac tat cac ctc cta aag gac cta gag	432
332	Tyr Asp Thr Ser Asp Ser Asp Asp Tyr His Leu Leu Lys Asp Leu Glu	
333	130 135 140	
335	gaa ggc atc caa acg ctg atg ggg gtg agg gtg gcg cca ggg gtc acc	480
336	Glu Gly Ile Gln Thr Leu Met Gly Val Arg Val Ala Pro Gly Val Thr	
337	145 150 155 160	
339	aat cct gga acc cca ctg gct tcg agg gct ggg gga gag aaa tac tgc	528
340	Asn Pro Gly Thr Pro Leu Ala Ser Arg Ala Gly Gly Glu Lys Tyr Cys	
341	165 170 175	
343	tgc cct ctt ttt agc agt aag gcg ctg acc caa gag aac tca cct tat	576
344	Cys Pro Leu Phe Ser Ser Lys Ala Leu Thr Gln Glu Asn Ser Pro Tyr	
345	180 185 190	
347	tct tca ttt cgc ctg gtg aat cct cca ggc ctt tct cta cac cct gaa	624
348	Ser Ser Phe Arg Leu Val Asn Pro Pro Gly Leu Ser Leu His Pro Glu	
349	195 200 205	
351	ggg gag gga gga aaa tgg ata aat gag aga ggg agg gaa cag tgc cca	672
352	Gly Glu Gly Gly Lys Trp Ile Asn Glu Arg Gly Arg Glu Gln Cys Pro	
353	210 215 220	
355	agc gct tgg cct ctc ctt ctc ttc ctt cac ttt gca gag gct gga aga	720
356	Ser Ala Trp Pro Leu Leu Leu Phe Leu His Phe Ala Glu Ala Gly Arg	
357	225 230 235 240	
359	cgg cag ccg ccg gac tgg gca gat cct caa gca gac cta cag caa gtt	768
360	Arg Gln Pro Pro Asp Trp Ala Asp Pro Gln Ala Asp Leu Gln Gln Val	
361	245 250 255	
363	tga caca aactcgacaca accatgacgc actgctcaag aactacgggc tgctctactg	825

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; N Pos. 8,38  
Seq#:28; N Pos. 1092  
Seq#:36; N Pos. 162,357  
Seq#:48; N Pos. 2817  
Seq#:56; N Pos. 34  
Seq#:78; N Pos. 1489,1491,1493  
Seq#:83; N Pos. 6,7,8  
Seq#:116; N Pos. 1  
Seq#:122; N Pos. 746  
Seq#:128; N Pos. 2247,2448,2449,2450,2451,2452,2457  
Seq#:133; N Pos. 1758  
Seq#:143; N Pos. 395  
Seq#:159; N Pos. 1980,2054  
Seq#:176; N Pos. 2851,2866  
Seq#:183; N Pos. 1952,1966  
Seq#:184; N Pos. 1622,1636,1644,1658  
Seq#:205; N Pos. 15,29,30,31  
Seq#:211; N Pos. 1582,1652  
Seq#:215; N Pos. 1923,1924,1925,1926,1927,1928,1929,1930,1931,1932,1933  
Seq#:215; N Pos. 1934,1935,1936,1937,1938,1939,1940,1941,1942,1943,1944  
Seq#:215; N Pos. 1945  
Seq#:223; N Pos. 6,7  
Seq#:239; N Pos. 818,823,836,847  
Seq#:242; N Pos. 2060  
Seq#:245; N Pos. 10  
Seq#:256; N Pos. 12,33,34,35,36,41  
Seq#:257; N Pos. 26  
Seq#:258; N Pos. 26  
Seq#:302; N Pos. 19,20,21  
Seq#:309; N Pos. 1081  
Seq#:319; N Pos. 22,29,59  
Seq#:326; N Pos. 290  
Seq#:331; N Pos. 19  
Seq#:372; N Pos. 756  
Seq#:378; N Pos. 1242  
Seq#:383; N Pos. 11  
Seq#:423; N Pos. 2600  
Seq#:452; N Pos. 1439,1441,1443  
Seq#:470; N Pos. 1823,1827,1866,1872,1876  
Seq#:535; N Pos. 587  
Seq#:549; N Pos. 1928  
Seq#:554; N Pos. 2013  
Seq#:599; N Pos. 6,37,38,205,231  
Seq#:602; N Pos. 13

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Seq#:605; N Pos. 3852,3857,3858,3896  
Seq#:607; N Pos. 3072,3073,3074,3075,3076,3077,3078,3079,3080,3081,3082  
Seq#:607; N Pos. 3083,3084,3085,3086,3087,3088,3089,3090,3091,3092,3093  
Seq#:607; N Pos. 3094,3095  
Seq#:651; N Pos. 7,8,9,10,11,12,28  
Seq#:1374; N Pos. 745,804,805,806,807,808,809,810,811,812,813,814,815,816  
Seq#:1374; N Pos. 817,818,819,820,821,822,823,824,825,826,827,828,829,830

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 80  
Seq#:2; Line(s) 160  
Seq#:8; Line(s) 831  
Seq#:13; Line(s) 1536  
Seq#:72; Line(s) 14760  
Seq#:79; Line(s) 16543  
Seq#:103; Line(s) 19937  
Seq#:107; Line(s) 20318  
Seq#:136; Line(s) 24652  
Seq#:144; Line(s) 25490  
Seq#:146; Line(s) 25777  
Seq#:149; Line(s) 26105  
Seq#:152; Line(s) 26553  
Seq#:165; Line(s) 28905  
Seq#:176; Line(s) 30637  
Seq#:231; Line(s) 40293  
Seq#:242; Line(s) 41573  
Seq#:246; Line(s) 42104  
Seq#:248; Line(s) 42353  
Seq#:279; Line(s) 47172  
Seq#:281; Line(s) 47535  
Seq#:296; Line(s) 50692  
Seq#:302; Line(s) 51385  
Seq#:305; Line(s) 51631  
Seq#:344; Line(s) 59516  
Seq#:345; Line(s) 59698  
Seq#:391; Line(s) 67770  
Seq#:398; Line(s) 69470  
Seq#:403; Line(s) 70930  
Seq#:404; Line(s) 71016  
Seq#:405; Line(s) 71080  
Seq#:406; Line(s) 71140  
Seq#:407; Line(s) 71176  
Seq#:494; Line(s) 82974  
Seq#:502; Line(s) 83910  
Seq#:523; Line(s) 87097  
Seq#:557; Line(s) 91904



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Seq#:575; Line(s) 94124  
Seq#:585; Line(s) 95177  
Seq#:618; Line(s) 100872  
Seq#:619; Line(s) 100915  
Seq#:632; Line(s) 103684  
Seq#:636; Line(s) 104084  
Seq#:640; Line(s) 104587  
Seq#:658; Line(s) 106533  
Seq#:664; Line(s) 107555  
Seq#:682; Line(s) 110706  
Seq#:1974; Line(s) 181376  
Seq#:1979; Line(s) 181553  
Seq#:1985; Line(s) 181762  
Seq#:1996; Line(s) 182183

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Input Set : D:\819\_seq\_listing.txt

Output Set: N:\CRF4\05032005\J531164.raw

L:30 M:270 C: Current Application Number differs, Replaced Current Application Number  
 L:31 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:2353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0  
 L:5287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:1052  
 L:7002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:120  
 M:341 Repeated in SeqNo=36  
 L:10403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:2779  
 L:11392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0  
 L:16518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:1443  
 L:16867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0  
 L:21495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116 after pos.:0  
 L:22142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:122 after pos.:692  
 L:22663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128 after pos.:2226  
 M:341 Repeated in SeqNo=128  
 L:24415 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:133 after pos.:1700  
 L:25471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:143 after pos.:353  
 L:27666 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:159 after pos.:1957  
 M:341 Repeated in SeqNo=159  
 L:30792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:176 after pos.:2804  
 M:341 Repeated in SeqNo=176  
 L:31875 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183 after pos.:1950  
 L:32013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:184 after pos.:1606  
 L:35212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:205 after pos.:0  
 L:36427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:211 after pos.:1542  
 M:341 Repeated in SeqNo=211  
 L:37350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215 after pos.:1872  
 M:341 Repeated in SeqNo=215  
 L:38267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:223 after pos.:0  
 L:41421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:239 after pos.:779  
 M:341 Repeated in SeqNo=239  
 L:41712 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:242 after pos.:2004  
 L:42009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:245 after pos.:0  
 L:43089 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:256 after pos.:0  
 L:43297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:257 after pos.:0  
 L:43479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:258 after pos.:0  
 L:51385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:302 after pos.:0  
 L:52515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:309 after pos.:1053  
 L:54937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:319 after pos.:0  
 L:56587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:326 after pos.:248  
 L:57108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:331 after pos.:0  
 L:65109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:372 after pos.:724  
 L:65867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:378 after pos.:1213  
 L:66590 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:383 after pos.:0  
 L:73889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:423 after pos.:2557  
 L:77743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:452 after pos.:1386  
 L:79945 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:470 after pos.:1795  
 M:341 Repeated in SeqNo=470  
 L:88570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:535 after pos.:553

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/531,164

DATE: 05/03/2005

TIME: 11:39:37

Input Set : D:\819\_seq\_listing.txt

Output Set: N:\CRF4\05032005\J531164.raw

L:90700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:549 after pos.:1897  
L:91380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:554 after pos.:1989  
L:96870 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:599 after pos.:0  
M:341 Repeated in SeqNo=599